

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

101689, 0821A

Source:

IFU 016

Date Processed by STIC:

11/6/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 11/08/2006

PATENT APPLICATION: US/10/689,082A

TIME: 13:16:41

Input Set : A:\Sequence_10-689,082.txt

Output Set: N:\CRF4\11082006\J689082A.raw

5 <110> APPLICANT: FOSTER, Timothy
 7 <120> TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCI

9 <130> FILE REFERENCE: P06335US04/BAS
 11 <140> CURRENT APPLICATION NUMBER: 10/689,082A
 12 <141> CURRENT FILING DATE: 2003-10-21
 14 <150> PRIOR APPLICATION NUMBER: 09/386,962
 15 <151> PRIOR FILING DATE: 1999-08-31
 17 <150> PRIOR APPLICATION NUMBER: 60/098,443
 18 <151> PRIOR FILING DATE: 1998-08-31
 20 <150> PRIOR APPLICATION NUMBER: 60/117,119
 21 <151> PRIOR FILING DATE: 1999-01-25
 23 <160> NUMBER OF SEQ ID NOS: 40
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 5406
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Staphylococcus epidermidis
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)..(5406)
 35 <223> OTHER INFORMATION:

W--> 37 <400> 1

38 tat tgg ata aat tat gct tat aaa gta ttt aca taa aaa tgt aaa tgc 48
 39 Tyr Trp Ile Asn Tyr Ala Tyr Lys Val Phe Thr Lys Cys Lys Cys
 40 1 5 10 15
 42 aat tta caa gta aat att caa att att tcc ttg taa aat att tat ttt 96
 43 Asn Leu Gln Val Asn Ile Gln Ile Ile Ser Leu Asn Ile Tyr Phe
 44 20 25 30
 46 aac tgg agg tat agt atg aaa aag aga aga caa gga cca att aac aag 144
 47 Asn Trp Arg Tyr Ser Met Lys Lys Arg Arg Gln Gly Pro Ile Asn Lys
 48 35 40 45
 50 aga gtg gat ttt cta tcc aac aag gta aac aag tac tcg att agg aag 192
 51 Arg Val Asp Phe Leu Ser Asn Lys Val Asn Lys Tyr Ser Ile Arg Lys
 52 50 55 60
 54 ttc aca gta ggt aca gct tca ata ctc gtg ggt gct acg tta atg ttt 240
 55 Phe Thr Val Gly Thr Ala Ser Ile Leu Val Gly Ala Thr Leu Met Phe
 56 65 70 75
 58 ggt gcc gca gac aat gag gct aaa gcg gct gaa gac aat caa tta gaa 288
 59 Gly Ala Ala Asp Asn Glu Ala Lys Ala Ala Glu Asp Asn Gln Leu Glu
 60 80 85 90
 62 tca gct tca aaa gaa gaa cag aaa ggt agt cgt gat aat gaa aac tca 336
 63 Ser Ala Ser Lys Glu Glu Gln Lys Gly Ser Arg Asp Asn Glu Asn Ser
 64 95 100 105 110

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66	aaa	ctt	aat	caa	gtc	gat	tta	gac	aac	gga	tca	cat	agt	tct	gag	aaa	384
67	Lys	Leu	Asn	Gln	Val	Asp	Leu	Asp	Asn	Gly	Ser	His	Ser	Ser	Glu	Lys	
68					115					120					125		
70	aca	aca	aat	gta	aac	aat	gca	act	gaa	gta	aaa	aaa	ggt	gaa	gca	cca	432
71	Thr	Thr	Asn	Val	Asn	Asn	Ala	Thr	Glu	Val	Lys	Lys	Val	Glu	Ala	Pro	
72				130					135					140			
74	acg	aca	agt	gac	gta	tct	aag	cct	aaa	gct	aat	gaa	gca	gta	gtg	acg	480
75	Thr	Thr	Ser	Asp	Val	Ser	Lys	Pro	Lys	Ala	Asn	Glu	Ala	Val	Val	Thr	
76			145				150					155					
78	aat	gag	tca	act	aaa	cca	aaa	aca	aca	gaa	gca	cca	act	ggt	aat	gag	528
79	Asn	Glu	Ser	Thr	Lys	Pro	Lys	Thr	Thr	Glu	Ala	Pro	Thr	Val	Asn	Glu	
80		160					165					170					
82	gaa	tca	ata	gct	gaa	aca	ccc	aaa	acc	tca	act	aca	caa	caa	gat	tcg	576
83	Glu	Ser	Ile	Ala	Glu	Thr	Pro	Lys	Thr	Ser	Thr	Thr	Gln	Gln	Asp	Ser	
84	175				180					185				190			
86	act	gag	aag	aat	aat	cca	tct	tta	aaa	gat	aat	tta	aat	tca	tcc	tca	624
87	Thr	Glu	Lys	Asn	Asn	Pro	Ser	Leu	Lys	Asp	Asn	Leu	Asn	Ser	Ser	Ser	
88			195				200					205					
90	acg	aca	tct	aaa	gaa	agt	aaa	aca	gac	gaa	cat	tct	act	aag	caa	gct	672
91	Thr	Thr	Ser	Lys	Glu	Ser	Lys	Thr	Asp	Glu	His	Ser	Thr	Lys	Gln	Ala	
92			210				215					220					
94	caa	atg	tct	act	aat	aaa	tca	aat	tta	gac	aca	aat	gac	tct	cca	act	720
95	Gln	Met	Ser	Thr	Asn	Lys	Ser	Asn	Leu	Asp	Thr	Asn	Asp	Ser	Pro	Thr	
96		225					230					235					
98	caa	agt	gag	aaa	act	tca	tca	caa	gca	aat	aac	gac	agt	aca	gat	aat	768
99	Gln	Ser	Glu	Lys	Thr	Ser	Ser	Gln	Ala	Asn	Asn	Asp	Ser	Thr	Asp	Asn	
100		240					245					250					
102	cag	tca	gca	cct	tct	aaa	caa	tta	gat	tca	aaa	cca	tca	gaa	caa	aaa	816
103	Gln	Ser	Ala	Pro	Ser	Lys	Gln	Leu	Asp	Ser	Lys	Pro	Ser	Glu	Gln	Lys	
104	255				260					265				270			
106	gta	tat	aaa	aca	aaa	ttt	aat	gat	gaa	cct	act	caa	gat	ggt	gaa	cac	864
107	Val	Tyr	Lys	Thr	Lys	Phe	Asn	Asp	Glu	Pro	Thr	Gln	Asp	Val	Glu	His	
108			275						280			285					
110	acg	aca	act	aaa	tta	aaa	aca	cct	tct	ggt	tca	aca	gat	agt	tca	gtc	912
111	Thr	Thr	Thr	Lys	Leu	Lys	Thr	Pro	Ser	Val	Ser	Thr	Asp	Ser	Ser	Val	
112			290				295					300					
114	aat	gat	aag	caa	gat	tac	aca	cga	agt	gct	gta	gct	agt	tta	ggt	ggt	960
115	Asn	Asp	Lys	Gln	Asp	Tyr	Thr	Arg	Ser	Ala	Val	Ala	Ser	Leu	Gly	Val	
116		305					310					315					
118	gat	tct	aat	gaa	aca	gaa	gca	att	aca	aat	gca	ggt	aga	gac	aat	tta	1008
119	Asp	Ser	Asn	Glu	Thr	Glu	Ala	Ile	Thr	Asn	Ala	Val	Arg	Asp	Asn	Leu	
120		320					325					330					
122	gat	tta	aaa	gct	gca	tct	aga	gaa	caa	atc	aat	gaa	gca	atc	att	gct	1056
123	Asp	Leu	Lys	Ala	Ala	Ser	Arg	Glu	Gln	Ile	Asn	Glu	Ala	Ile	Ile	Ala	
124	335				340					345				350			
126	gaa	gca	cta	aaa	aaa	gac	ttt	tct	aac	cct	gat	tat	ggt	gtc	gat	acg	1104
127	Glu	Ala	Leu	Lys	Lys	Asp	Phe	Ser	Asn	Pro	Asp	Tyr	Gly	Val	Asp	Thr	
128			355				360					365					
130	cca	tta	gct	cta	aac	aga	tct	caa	tca	aaa	aat	tca	cca	cat	aag	agt	1152

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131	Pro	Leu	Ala	Leu	Asn	Arg	Ser	Gln	Ser	Lys	Asn	Ser	Pro	His	Lys	Ser	
132				370					375					380			
134	gca	agt	cca	cgc	atg	aat	tta	atg	agt	tta	gct	gct	gag	cct	aat	agt	1200
135	Ala	Ser	Pro	Arg	Met	Asn	Leu	Met	Ser	Leu	Ala	Ala	Glu	Pro	Asn	Ser	
136			385					390					395				
138	ggt	aaa	aat	gtg	aat	gat	aaa	ggt	aaa	atc	aca	aac	cct	acg	ctt	tca	1248
139	Gly	Lys	Asn	Val	Asn	Asp	Lys	Val	Lys	Ile	Thr	Asn	Pro	Thr	Leu	Ser	
140		400					405					410					
142	ctt	aat	aag	agt	aat	aat	cac	gct	aat	aac	gta	ata	tgg	cca	aca	agt	1296
143	Leu	Asn	Lys	Ser	Asn	Asn	His	Ala	Asn	Asn	Val	Ile	Trp	Pro	Thr	Ser	
144	415				420					425					430		
146	aac	gaa	caa	ttt	aat	tta	aaa	gca	aat	tat	gaa	tta	gat	gac	agc	ata	1344
147	Asn	Glu	Gln	Phe	Asn	Leu	Lys	Ala	Asn	Tyr	Glu	Leu	Asp	Asp	Ser	Ile	
148				435					440					445			
150	aaa	gag	gga	gat	act	ttt	act	att	aag	tat	ggt	cag	tat	att	aga	ccg	1392
151	Lys	Glu	Gly	Asp	Thr	Phe	Thr	Ile	Lys	Tyr	Gly	Gln	Tyr	Ile	Arg	Pro	
152			450					455				460					
154	ggt	ggt	tta	gaa	ctt	cct	gca	ata	aaa	act	caa	cta	cgt	agt	aag	gat	1440
155	Gly	Gly	Leu	Glu	Leu	Pro	Ala	Ile	Lys	Thr	Gln	Leu	Arg	Ser	Lys	Asp	
156		465				470					475						
158	ggc	tct	att	gta	gct	aat	ggt	gta	tat	gat	aaa	act	aca	aat	acg	acg	1488
159	Gly	Ser	Ile	Val	Ala	Asn	Gly	Val	Tyr	Asp	Lys	Thr	Thr	Asn	Thr	Thr	
160		480				485					490						
162	act	tat	aca	ttt	act	aac	tat	ggt	gat	caa	tat	caa	aat	att	aca	ggt	1536
163	Thr	Tyr	Thr	Phe	Thr	Asn	Tyr	Val	Asp	Gln	Tyr	Gln	Asn	Ile	Thr	Gly	
164	495				500					505				510			
166	agt	ttt	gat	tta	att	gcg	acg	cct	aag	agg	gaa	aca	gca	att	aag	gat	1584
167	Ser	Phe	Asp	Leu	Ile	Ala	Thr	Pro	Lys	Arg	Glu	Thr	Ala	Ile	Lys	Asp	
168				515					520					525			
170	aat	cag	aat	tat	cct	atg	gaa	gtg	acg	att	gct	aac	gaa	gta	gtc	aaa	1632
171	Asn	Gln	Asn	Tyr	Pro	Met	Glu	Val	Thr	Ile	Ala	Asn	Glu	Val	Val	Lys	
172			530					535				540					
174	aaa	gac	ttc	att	gtg	gat	tat	ggt	aat	aaa	aag	gac	aat	aca	act	aca	1680
175	Lys	Asp	Phe	Ile	Val	Asp	Tyr	Gly	Asn	Lys	Lys	Asp	Asn	Thr	Thr	Thr	
176		545				550					555						
178	gca	gcg	gta	gca	aat	gtg	gat	aat	gta	aat	aat	aaa	cat	aac	gaa	gtt	1728
179	Ala	Ala	Val	Ala	Asn	Val	Asp	Asn	Val	Asn	Asn	Lys	His	Asn	Glu	Val	
180		560				565					570						
182	gtt	tat	cta	aac	caa	aat	aac	caa	aac	cct	aaa	tat	gct	aaa	tat	ttc	1776
183	Val	Tyr	Leu	Asn	Gln	Asn	Asn	Gln	Asn	Pro	Lys	Tyr	Ala	Lys	Tyr	Phe	
184	575				580					585					590		
186	tca	aca	gta	aaa	aat	ggt	gaa	ttt	ata	cca	ggt	gaa	gtg	aaa	gtt	tac	1824
187	Ser	Thr	Val	Lys	Asn	Gly	Glu	Phe	Ile	Pro	Gly	Glu	Val	Lys	Val	Tyr	
188				595				600				605					
190	gaa	gtg	acg	gat	acc	aat	gcg	atg	gta	gat	agc	ttc	aat	cct	gat	tta	1872
191	Glu	Val	Thr	Asp	Thr	Asn	Ala	Met	Val	Asp	Ser	Phe	Asn	Pro	Asp	Leu	
192			610					615				620					
194	aat	agt	tct	aat	gta	aaa	gat	gtg	aca	agt	caa	ttt	gca	cct	aaa	gta	1920
195	Asn	Ser	Ser	Asn	Val	Lys	Asp	Val	Thr	Ser	Gln	Phe	Ala	Pro	Lys	Val	

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196	625	630	635	
198	agt gca gat ggt act aga gtt gat atc aat ttt gct aga agt atg gca	1968		
199	Ser Ala Asp Gly Thr Arg Val Asp Ile Asn Phe Ala Arg Ser Met Ala			
200	640 645 650			
202	aat ggt aaa aag tat att gta act caa gca gtg aga cca acg gga act	2016		
203	Asn Gly Lys Lys Tyr Ile Val Thr Gln Ala Val Arg Pro Thr Gly Thr			
204	655 660 665 670			
206	gga aat gtt tat acc gaa tat tgg tta aca aga gat ggt act acc aat	2064		
207	Gly Asn Val Tyr Thr Glu Tyr Trp Leu Thr Arg Asp Gly Thr Thr Asn			
208	675 680 685			
210	aca aat gat ttt tac cgt gga acg aag tct aca acg gtg act tat ctc	2112		
211	Thr Asn Asp Phe Tyr Arg Gly Thr Lys Ser Thr Thr Val Thr Tyr Leu			
212	690 695 700			
214	aat ggt tct tca aca gca cag ggg gat aat cct aca tat agt cta ggt	2160		
215	Asn Gly Ser Ser Thr Ala Gln Gly Asp Asn Pro Thr Tyr Ser Leu Gly			
216	705 710 715			
218	gac tat gta tgg tta gat aaa aat aaa aac ggt gtt caa gat gat gat	2208		
219	Asp Tyr Val Trp Leu Asp Lys Asn Lys Asn Gly Val Gln Asp Asp Asp			
220	720 725 730			
222	gag aaa ggt tta gca ggt gtt tat gtt act ctt aaa gac agt aac aat	2256		
223	Glu Lys Gly Leu Ala Gly Val Tyr Val Thr Leu Lys Asp Ser Asn Asn			
224	735 740 745 750			
226	aga gaa tta caa cgt gta act act gat caa tct gga cat tat caa ttt	2304		
227	Arg Glu Leu Gln Arg Val Thr Thr Asp Gln Ser Gly His Tyr Gln Phe			
228	755 760 765			
230	gat aat tta caa aat gga acg tac aca gtc gag ttt gcg att cct gat	2352		
231	Asp Asn Leu Gln Asn Gly Thr Tyr Thr Val Glu Phe Ala Ile Pro Asp			
232	770 775 780			
234	aat tat acg cca tct ccc gca aat aat tct aca aat gat gca ata gat	2400		
235	Asn Tyr Thr Pro Ser Pro Ala Asn Asn Ser Thr Asn Asp Ala Ile Asp			
236	785 790 795			
238	tca gat ggt gaa cgt gat ggt aca cgt aaa gta gtt gtt gcc aaa gga	2448		
239	Ser Asp Gly Glu Arg Asp Gly Thr Arg Lys Val Val Val Ala Lys Gly			
240	800 805 810			
242	aca att aat aat gct gat aat atg act gta gat act ggc ttt tat tta	2496		
243	Thr Ile Asn Asn Ala Asp Asn Met Thr Val Asp Thr Gly Phe Tyr Leu			
244	815 820 825 830			
246	act cct aaa tac aat gtc gga gat tat gta tgg gaa gat aca aat aaa	2544		
247	Thr Pro Lys Tyr Asn Val Gly Asp Tyr Val Trp Glu Asp Thr Asn Lys			
248	835 840 845			
250	gat ggt atc caa gat gac aat gaa aaa gga att tct ggt gtt aaa gta	2592		
251	Asp Gly Ile Gln Asp Asp Asn Glu Lys Gly Ile Ser Gly Val Lys Val			
252	850 855 860			
254	acg tta aaa aat aaa aat gga gat act att ggc aca acg aca aca gat	2640		
255	Thr Leu Lys Asn Lys Asn Gly Asp Thr Ile Gly Thr Thr Thr Asp			
256	865 870 875			
258	tca aat ggt aaa tat gaa ttc aca ggt tta gag aac ggg gat tac aca	2688		
259	Ser Asn Gly Lys Tyr Glu Phe Thr Gly Leu Glu Asn Gly Asp Tyr Thr			
260	880 885 890			

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262	ata gaa ttt gag acg ccg gaa ggc tac aca ccg act aaa caa aac tcg	2736
263	Ile Glu Phe Glu Thr Pro Glu Gly Tyr Thr Pro Thr Lys Gln Asn Ser	
264	895 900 905 910	
266	gga agt gac gaa ggt aaa gat tca aac ggt acg aaa aca aca gtc aca	2784
267	Gly Ser Asp Glu Gly Lys Asp Ser Asn Gly Thr Lys Thr Thr Val Thr	
268	915 920 925	
270	gtc aaa gat gca gat aat aaa aca ata gac tca ggt ttc tac aag cca	2832
271	Val Lys Asp Ala Asp Asn Lys Thr Ile Asp Ser Gly Phe Tyr Lys Pro	
272	930 935 940	
274	aca tat aac tta ggt gac tat gta tgg gaa gat aca aat aaa gat ggt	2880
275	Thr Tyr Asn Leu Gly Asp Tyr Val Trp Glu Asp Thr Asn Lys Asp Gly	
276	945 950 955	
278	att caa gac gac agt gaa aaa ggg att tct ggg gtt aaa gtg acg tta	2928
279	Ile Gln Asp Asp Ser Glu Lys Gly Ile Ser Gly Val Lys Val Thr Leu	
280	960 965 970	
282	aaa gat aaa aat gga aat gcc att ggg aca acg aca aca gac gca agt	2976
283	Lys Asp Lys Asn Gly Asn Ala Ile Gly Thr Thr Thr Thr Asp Ala Ser	
284	975 980 985 990	
286	ggt cat tat caa ttt aaa gga tta gaa aat gga agc tac aca gtt gag	3024
287	Gly His Tyr Gln Phe Lys Gly Leu Glu Asn Gly Ser Tyr Thr Val Glu	
288	995 1000 1005	
290	ttt gag aca cca tca ggt tat aca ccg aca aaa gcg aat tca ggt	3069
291	Phe Glu Thr Pro Ser Gly Tyr Thr Pro Thr Lys Ala Asn Ser Gly	
292	1010 1015 1020	
294	caa gat ata act gta gat tcc aac ggt ata aca aca aca ggt atc	3114
295	Gln Asp Ile Thr Val Asp Ser Asn Gly Ile Thr Thr Thr Gly Ile	
296	1025 1030 1035	
298	att aac gga gct gat aat ctc aca att gat agt ggt ttc tac aaa	3159
299	Ile Asn Gly Ala Asp Asn Leu Thr Ile Asp Ser Gly Phe Tyr Lys	
300	1040 1045 1050	
302	aca cca aaa tat agt gtc gga gat tat gta tgg gaa gat aca aat	3204
303	Thr Pro Lys Tyr Ser Val Gly Asp Tyr Val Trp Glu Asp Thr Asn	
304	1055 1060 1065	
306	aaa gat ggt atc caa gat gac aat gaa aag gga att tct ggt gtt	3249
307	Lys Asp Gly Ile Gln Asp Asp Asn Glu Lys Gly Ile Ser Gly Val	
308	1070 1075 1080	
310	aaa gta acg tta aag gat gaa aaa gga aat ata att agc act aca	3294
311	Lys Val Thr Leu Lys Asp Glu Lys Gly Asn Ile Ile Ser Thr Thr	
312	1085 1090 1095	
314	aca act gat gaa aat ggg aag tat caa ttt gat aat tta gat agt	3339
315	Thr Thr Asp Glu Asn Gly Lys Tyr Gln Phe Asp Asn Leu Asp Ser	
316	1100 1105 1110	
318	ggt aat tac att att cat ttt gag aaa ccg gaa ggc atg act caa	3384
319	Gly Asn Tyr Ile Ile His Phe Glu Lys Pro Glu Gly Met Thr Gln	
320	1115 1120 1125	
322	act aca gca aat tct gga aat gat gat gaa aaa gat gct gat ggg	3429
323	Thr Thr Ala Asn Ser Gly Asn Asp Asp Glu Lys Asp Ala Asp Gly	
324	1130 1135 1140	
326	gaa gat gtt cgt gtt acg att act gat cat gat gac ttt agt ata	3474

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/08/2006
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 6,12

Seq#:17; Xaa Pos. 3

VERIFICATION SUMMARY

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L:37 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35
L:903 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:901
L:1452 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:1450
L:1725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:1751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0